

## SEQUENCE LISTING

<110> Oregon Health & Science University  
 Moses, Ashlee  
 Nelson, Jay  
 Fruh, Klaus  
 King, Jeff  
 Jelinek, Laura  
 Hirsch, Alec  
 DeFilippis, Victor

<120> METHODS OF TREATMENT AND DIAGNOSIS USING MODULATORS OF  
 VIRUS-INDUCED CELLULAR GENE SEQUENCES

<130> 899-73077-04

<140> US

<141> 2004-04-15

<150> PCT/US2004/011988

<151> 2004-04-15

<150> US 60/486,694

<151> 2003-07-11

<150> US 60/533,103

<151> 2003-12-29

<160> 17

<170> PatentIn version 3.2

<210> 1

<211> 1232

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (19)..(1044)

<400> 1

tttccc	gaga	tcaccaag	atg	ctg	ggc	gcc	gag	tgg	agc	aag	ctg	cag	cca	51
			Met	Leu	Gly	Ala	Glu	Trp	Ser	Lys	Leu	Gln	Pro	
			1				5					10		

acg	gaa	aag	cag	cgg	tac	ctg	gat	gag	gcc	gag	aga	gag	aag	cag	cag	99
Thr	Glu	Lys	Gln	Arg	Tyr	Leu	Asp	Glu	Ala	Glu	Arg	Glu	Lys	Gln	Gln	
			15					20					25			

tac	atg	aag	gag	ctg	cgg	gcg	tac	cag	cag	tct	gaa	gcc	tat	aag	atg	147
Tyr	Met	Lys	Glu	Leu	Arg	Ala	Tyr	Gln	Gln	Ser	Glu	Ala	Tyr	Lys	Met	
			30				35					40				

tgc	acg	gag	aag	atc	cag	gag	aag	aag	atc	aag	aaa	gaa	gac	tcg	agc	195
Cys	Thr	Glu	Lys	Ile	Gln	Glu	Lys	Lys	Ile	Lys	Lys	Glu	Asp	Ser	Ser	

45	50	55	
tct ggg ctc atg aac act ctc ctg aat gga cac aag ggt ggg gac tgc			243
Ser Gly Leu Met Asn Thr Leu Leu Asn Gly His Lys Gly Gly Asp Cys			
60	65	70	75
gat ggc ttc tcc acc ttc gat gtt ccc atc ttc act gaa gag ttc ttg			291
Asp Gly Phe Ser Thr Phe Asp Val Pro Ile Phe Thr Glu Glu Phe Leu			
	80	85	90
gac caa aac aaa gcg cgt gag gcg gag ctt cgg cgc ttg cgg aag atg			339
Asp Gln Asn Lys Ala Arg Glu Ala Glu Leu Arg Arg Leu Arg Lys Met			
	95	100	105
aat gtg gcc ttc gag gag cag aac gcg gta ctg cag agg caa aac gca			387
Asn Val Ala Phe Glu Glu Gln Asn Ala Val Leu Gln Arg Gln Asn Ala			
	110	115	120
gag cat gag cag cgc gcg cga gcg tct gga gca gga gct ggc gct gga			435
Glu His Glu Gln Arg Ala Arg Ala Ser Gly Ala Gly Ala Gly Ala Gly			
	125	130	135
gga gcg gag gac gct ggc gct gca gca gca gct cca ggc cgt gcg cca			483
Gly Ala Glu Asp Ala Gly Ala Ala Ala Ala Ala Pro Gly Arg Ala Pro			
	140	145	150
ggc gct cac cgc cag ctt cgc ctc act gcc ggt gcc ggg cac ggg cga			531
Gly Ala His Arg Gln Leu Arg Leu Thr Ala Gly Ala Gly His Gly Arg			
	160	165	170
aac gcc cac gct ggg cac tct gga ctt cta cat ggc ccg gct tca cgg			579
Asn Ala His Ala Gly His Ser Gly Leu Leu His Gly Pro Ala Ser Arg			
	175	180	185
agc cat cga gcg cga ccc cgc cca gca cga gaa gct cat cgt ccg cat			627
Ser His Arg Ala Arg Pro Arg Pro Ala Arg Glu Ala His Arg Pro His			
	190	195	200
caa gga aat cct ggc cca ggt cgc cag cga gca cct gtg agg agt ggg			675
Gln Gly Asn Pro Gly Pro Gly Arg Gln Arg Ala Pro Val Arg Ser Gly			
	205	210	215
cgg gcc cac gat gca gag gag aag ctg tgg gcg cgg ccc tgc cac acc			723
Arg Ala His Asp Ala Glu Glu Lys Leu Trp Ala Arg Pro Cys His Thr			
	220	225	230
cca ccc cgt gga cga gag gct ggg ggt cca ccc ttt ggg gcc tgg tcc			771
Pro Pro Arg Gly Arg Glu Ala Gly Gly Pro Pro Phe Gly Ala Trp Ser			
	240	245	250
cat cct gca cct ttg ggg gct cca gcc ccc cta aaa tta aat ttc tgc			819
His Pro Ala Pro Leu Gly Ala Pro Ala Pro Leu Lys Leu Asn Phe Cys			
	255	260	265
agc atc cct tta gct ttc aat ctc ccc agc ccc ctg aac ccg gaa aaa			867
Ser Ile Pro Leu Ala Phe Asn Leu Pro Ser Pro Leu Asn Pro Glu Lys			
	270	275	280

gca ctc gct gcg cga tac acc cag aag aac ctc aca gcc gag ggt gcc	915
Ala Leu Ala Ala Arg Tyr Thr Gln Lys Asn Leu Thr Ala Glu Gly Ala	
285 290 295	

cct cct cgg agg aca gcc acg cgc tac act ggc tct ccg ggc cac ccc	963
Pro Pro Arg Arg Thr Ala Thr Arg Tyr Thr Gly Ser Pro Gly His Pro	
300 305 310 315	

cag gac aca ggg cag acg aaa ccc acc ccc agc aca cgg cag gac ccc	1011
Gln Asp Thr Gly Gln Thr Lys Pro Thr Pro Ser Thr Arg Gln Asp Pro	
320 325 330	

cca aat tac tca cta cgg ggg gct gtg cca tag gccacacagg aagctgcctt	1064
Pro Asn Tyr Ser Leu Arg Gly Ala Val Pro	
335 340	

gtgggggactt acctgggggtg tccccgcgat gcctgtaccc cagatgggtg gggggccggct	1124
--	------

ttgcccattcc tgctctctc cagccgaggg accctgggtg ggggtggctcc ttctcactgc	1184
--	------

tggatccgga ctttttaaataaaaaacaagt aaaatttgtg ttttaaaa	1232
--	------

<210> 2  
 <211> 341  
 <212> PRT  
 <213> Homo sapiens

<400> 2

Met Leu Gly Ala Glu Trp Ser Lys Leu Gln Pro Thr Glu Lys Gln Arg
1 5 10 15

Tyr Leu Asp Glu Ala Glu Arg Glu Lys Gln Gln Tyr Met Lys Glu Leu
20 25 30

Arg Ala Tyr Gln Gln Ser Glu Ala Tyr Lys Met Cys Thr Glu Lys Ile
35 40 45

Gln Glu Lys Lys Ile Lys Lys Glu Asp Ser Ser Ser Gly Leu Met Asn
50 55 60

Thr Leu Leu Asn Gly His Lys Gly Gly Asp Cys Asp Gly Phe Ser Thr
65 70 75 80

Phe Asp Val Pro Ile Phe Thr Glu Glu Phe Leu Asp Gln Asn Lys Ala
85 90 95

Arg Glu Ala Glu Leu Arg Arg Leu Arg Lys Met Asn Val Ala Phe Glu
100 105 110

Glu Gln Asn Ala Val Leu Gln Arg Gln Asn Ala Glu His Glu Gln Arg  
115 120 125

Ala Arg Ala Ser Gly Ala Gly Ala Gly Ala Gly Ala Glu Asp Ala  
130 135 140

Gly Ala Ala Ala Ala Ala Pro Gly Arg Ala Pro Gly Ala His Arg Gln  
145 150 155 160

Leu Arg Leu Thr Ala Gly Ala Gly His Gly Arg Asn Ala His Ala Gly  
165 170 175

His Ser Gly Leu Leu His Gly Pro Ala Ser Arg Ser His Arg Ala Arg  
180 185 190

Pro Arg Pro Ala Arg Glu Ala His Arg Pro His Gln Gly Asn Pro Gly  
195 200 205

Pro Gly Arg Gln Arg Ala Pro Val Arg Ser Gly Arg Ala His Asp Ala  
210 215 220

Glu Glu Lys Leu Trp Ala Arg Pro Cys His Thr Pro Pro Arg Gly Arg  
225 230 235 240

Glu Ala Gly Gly Pro Pro Phe Gly Ala Trp Ser His Pro Ala Pro Leu  
245 250 255

Gly Ala Pro Ala Pro Leu Lys Leu Asn Phe Cys Ser Ile Pro Leu Ala  
260 265 270

Phe Asn Leu Pro Ser Pro Leu Asn Pro Glu Lys Ala Leu Ala Ala Arg  
275 280 285

Tyr Thr Gln Lys Asn Leu Thr Ala Glu Gly Ala Pro Pro Arg Arg Thr  
290 295 300

Ala Thr Arg Tyr Thr Gly Ser Pro Gly His Pro Gln Asp Thr Gly Gln  
305 310 315 320

Thr Lys Pro Thr Pro Ser Thr Arg Gln Asp Pro Pro Asn Tyr Ser Leu  
325 330 335

Arg Gly Ala Val Pro  
340

<210> 3  
<211> 3870  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (179)..(1642)

<400> 3  
cagggagaca tacaggattt aagaagccca tcatggagaa gaccttcaat tacagagata 60  
aaaagttttt cttgtggaac aagttaacac tagatggcag ataacagact gaggagtgag 120  
ctgcttctga ctcgattaaa aagggagtga gccataactg gcggctgctc tttcgcca 178  
atg agc ctc ccc aat tcc tcc tgc ctc tta gaa gac aag atg tgt gag 226  
Met Ser Leu Pro Asn Ser Ser Cys Leu Leu Glu Asp Lys Met Cys Glu  
1 5 10 15  
ggc aac aag acc act atg gcc agc ccc cag ctg atg ccc ctg gtg gtg 274  
Gly Asn Lys Thr Thr Met Ala Ser Pro Gln Leu Met Pro Leu Val Val  
20 25 30  
gtc ctg agc act atc tgc ttg gtc aca gta ggg ctc aac ctg ctg gtg 322  
Val Leu Ser Thr Ile Cys Leu Val Thr Val Gly Leu Asn Leu Leu Val  
35 40 45  
ctg tat gcc gta cgg agt gag cgg aag ctc cac act gtg ggg aac ctg 370  
Leu Tyr Ala Val Arg Ser Glu Arg Lys Leu His Thr Val Gly Asn Leu  
50 55 60  
tac atc gtc agc ctc tcg gtg gcg gac ttg atc gtg ggt gcc gtc gtc 418  
Tyr Ile Val Ser Leu Ser Val Ala Asp Leu Ile Val Gly Ala Val Val  
65 70 75 80  
atg cct atg aac atc ctc tac ctg ctc atg tcc aag tgg tca ctg ggc 466  
Met Pro Met Asn Ile Leu Tyr Leu Leu Met Ser Lys Trp Ser Leu Gly  
85 90 95  
cgt cct ctc tgc ctc ttt tgg ctt tcc atg gac tat gtg gcc agc aca 514  
Arg Pro Leu Cys Leu Phe Trp Leu Ser Met Asp Tyr Val Ala Ser Thr  
100 105 110  
gcg tcc att ttc agt gtc ttc atc ctg tgc att gat cgc tac cgc tct 562  
Ala Ser Ile Phe Ser Val Phe Ile Leu Cys Ile Asp Arg Tyr Arg Ser  
115 120 125  
gtc cag cag ccc ctc agg tac ctt aag tat cgt acc aag acc cga gcc 610  
Val Gln Gln Pro Leu Arg Tyr Leu Lys Tyr Arg Thr Lys Thr Arg Ala  
130 135 140

tcg gcc acc att ctg ggg gcc tgg ttt ctc tct ttt ctg tgg gtt att	658
Ser Ala Thr Ile Leu Gly Ala Trp Phe Leu Ser Phe Leu Trp Val Ile	
145 150 155 160	
ccc att cta ggc tgg aat cac ttc atg cag cag acc tcg gtg cgc cga	706
Pro Ile Leu Gly Trp Asn His Phe Met Gln Gln Thr Ser Val Arg Arg	
165 170 175	
gag gac aag tgt gag aca gac ttc tat gat gtc acc tgg ttc aag gtc	754
Glu Asp Lys Cys Glu Thr Asp Phe Tyr Asp Val Thr Trp Phe Lys Val	
180 185 190	
atg act gcc atc atc aac ttc tac ctg ccc acc ttg ctc atg ctc tgg	802
Met Thr Ala Ile Ile Asn Phe Tyr Leu Pro Thr Leu Leu Met Leu Trp	
195 200 205	
ttc tat gcc aag atc tac aag gcc gta cga caa cac tgc cag cac cgg	850
Phe Tyr Ala Lys Ile Tyr Lys Ala Val Arg Gln His Cys Gln His Arg	
210 215 220	
gag ctc atc aat agg tcc ctc cct tcc ttc tca gaa att aag ctg agg	898
Glu Leu Ile Asn Arg Ser Leu Pro Ser Phe Ser Glu Ile Lys Leu Arg	
225 230 235 240	
cca gag aac ccc aag ggg gat gcc aag aaa cca ggg aag gag tct ccc	946
Pro Glu Asn Pro Lys Gly Asp Ala Lys Lys Pro Gly Lys Glu Ser Pro	
245 250 255	
tgg gag gtt ctg aaa agg aag cca aaa gat gct ggt ggt gga tct gtc	994
Trp Glu Val Leu Lys Arg Lys Pro Lys Asp Ala Gly Gly Gly Ser Val	
260 265 270	
ttg aag tca cca tcc caa acc ccc aag gag atg aaa tcc cca gtt gtc	1042
Leu Lys Ser Pro Ser Gln Thr Pro Lys Glu Met Lys Ser Pro Val Val	
275 280 285	
ttc agc caa gag gat gat aga gaa gta gac aaa ctc tac tgc ttt cca	1090
Phe Ser Gln Glu Asp Asp Arg Glu Val Asp Lys Leu Tyr Cys Phe Pro	
290 295 300	
ctt gat att gtg cac atg cag gct gcg gca gag ggg agt agc agg gac	1138
Leu Asp Ile Val His Met Gln Ala Ala Ala Glu Gly Ser Ser Arg Asp	
305 310 315 320	
tat gta gcc gtc aac cgg agc cat ggc cag ctc aag aca gat gag cag	1186
Tyr Val Ala Val Asn Arg Ser His Gly Gln Leu Lys Thr Asp Glu Gln	
325 330 335	
ggc ctg aac aca cat ggg gcc agc gag ata tca gag gat cag atg tta	1234
Gly Leu Asn Thr His Gly Ala Ser Glu Ile Ser Glu Asp Gln Met Leu	
340 345 350	
ggt gat agc caa tcc ttc tct cga acg gac tca gat acc acc aca gag	1282
Gly Asp Ser Gln Ser Phe Ser Arg Thr Asp Ser Asp Thr Thr Thr Glu	
355 360 365	

aca gca cca ggc aaa ggc aaa ttg agg agt ggg tct aac aca ggc ctg Thr Ala Pro Gly Lys Gly Lys Leu Arg Ser Gly Ser Asn Thr Gly Leu 370 375 380	1330
gat tac atc aag ttt act tgg aag agg ctc cgc tcg cat tca aga cag Asp Tyr Ile Lys Phe Thr Trp Lys Arg Leu Arg Ser His Ser Arg Gln 385 390 395 400	1378
tat gta tct ggg ttg cac atg aac cgc gaa agg aag gcc gcc aaa cag Tyr Val Ser Gly Leu His Met Asn Arg Glu Arg Lys Ala Ala Lys Gln 405 410 415	1426
ttg ggt ttt atc atg gca gcc ttc atc ctc tgc tgg atc cct tat ttc Leu Gly Phe Ile Met Ala Ala Phe Ile Leu Cys Trp Ile Pro Tyr Phe 420 425 430	1474
atc ttc ttc atg gtc att gcc ttc tgc aag aac tgt tgc aat gaa cat Ile Phe Phe Met Val Ile Ala Phe Cys Lys Asn Cys Cys Asn Glu His 435 440 445	1522
ttg cac atg ttc acc atc tgg ctg ggc tac atc aac tcc aca ctg aac Leu His Met Phe Thr Ile Trp Leu Gly Tyr Ile Asn Ser Thr Leu Asn 450 455 460	1570
ccc ctc atc tac ccc ttg tgc aat gag aac ttc aag aag aca ttc aag Pro Leu Ile Tyr Pro Leu Cys Asn Glu Asn Phe Lys Lys Thr Phe Lys 465 470 475 480	1618
aga att ctg cat att cgc tcc taa gggaggctct gaggggatgc aacaaaatga Arg Ile Leu His Ile Arg Ser 485	1672
tccttatgat gtccaacaag gaaatagagg acgaaggcct gtgtgttgcc aggcaggcac	1732
ctgggctttc tggaatccaa accacagtct taggggcttg gtagtttgga aagttcttag	1792
gcaccataga agaacagcag atggcggtga tcagcagaga gattgaactt tgaggaggaa	1852
gcagaatctt tgcaagaaag tcagacctgt ttcttgtaac tgggttcaaa aagaaaaaaa	1912
taataaaaat aaaagagaga gagaatcaga cctgggtgga actctcctgc tcctcaggaa	1972
ctatgggagc ctcagactca ttgtaattca agctttccga gtcaagtgat tgacaactga	2032
agagacacgt ggctaggggt cactggaga attgaaaagg actcttgagc cctcctggaa	2092
tggagctgta taactgtgca gagactttat ccatgccaat agttgctgtc cccttcagg	2152
ggtcaccttg agaggcatga cagctgttcc acaggggcta tcccttctca gaaaacttct	2212
cttctgagcc tctttaacag ctttctccag aaccagtgtc tgaaccaccc tggaaattct	2272
gccttattat ttcttactca aacatgttta gagtggatag aaaattatgc agcttgaca	2332
cccatcatct ttaaccccaa atttcctttg gctattaaaa aagtgggtggc aaaaggcatc	2392
ctcaaaagaa agagaaatga aatatttttg aatgggtgca cgttaaaaat taaaagaagg	2452

aatgggggca gaatgccata tttttgaggg ctgtactagg tttatctcat ttaagcccca	2512
caacacccca caggagggta attttctaac tctagtttgc agaggagcaa attgaggttc	2572
agcaaggtga gagaggtacc caaggtcaca tagctagtta tgtgagaaag ttagagtaca	2632
gatcctctgg ggtttcagct tattgtagca tattttctcc gaaaggcaaa aatgtgccct	2692
tttgccggg catggtagct caagcctata atcccagcat gttgagaggc tgaggtgggc	2752
agatcatttg aggccaggag ttcaagacca gtctggccaa tatggagaaa ccttgtctct	2812
actaaaaaca caaaaattat ctgggcatgg tggggcatgc ctgtagtccc acttacttgg	2872
gaggccgagg cacgagaatc gcttgaaccc gggagggtga gggtgccgtg agccaagatc	2932
acgccactgc actccagcct gggcaacaga gcaagactct gtctcaaaaa aaaaaataca	2992
atattttaac aatgtgccct cttaagtgtg cacagataca catacacggt attcccaaga	3052
gtggtggcag ctcaaaatga tatgtttgag tagacgaaca gctgacatgg agttcccgtg	3112
cacctacgga aggggacgct ttgaaggaac caagtgcatt tttatctgtg agttctgttg	3172
tgtttgtcaa aaagtcattg taatctttca tagccatacc tggtaagcaa aaactagtaa	3232
agacatagga acatgtagtt ttacttggtg tttatgttgc aatctggttg tgatttatat	3292
tttaaagctt ggtgctaaac cacaatatgt atagcacatg gagtgcctgt acaagctgat	3352
gttttgtatt ttgtgttcct ctttgcata tctgtcaaag tgagatattt ttacctgcct	3412
aaaatatgat gtttaaaagc atactctatg tgatttatatt atttctacct ttctgagtct	3472
cttgactaa gaagatgttt tgaaatgtac catcaaatgt taacagagtt tgatatgggc	3532
tttctctttg gtttctcatc acatttgtaa atgtcttttc aaaaggattt actttttgta	3592
aaaagcttca ttctcactct gctttgcatc ccccaaactt cttgttcaaa acgggggggag	3652
tttaggagac tttaatcccg gtttcagaag ctgcagctgg tctgtttcca ggtcagaaac	3712
cattgttcag aagacctccc tgtgagagag ttgctcctca gggccctca ggaccaaaga	3772
acactcgaaa agagcacttc acacagacaa gtggctaagt gtccattatt taccttgaac	3832
aatcaaggca actagtggag agaactgatt gtgagctc	3870

<210> 4  
 <211> 487  
 <212> PRT  
 <213> Homo sapiens

<400> 4



Met Ser Leu Pro Asn Ser Ser Cys Leu Leu Glu Asp Lys Met Cys Glu  
1 5 10 15

Gly Asn Lys Thr Thr Met Ala Ser Pro Gln Leu Met Pro Leu Val Val  
20 25 30

Val Leu Ser Thr Ile Cys Leu Val Thr Val Gly Leu Asn Leu Leu Val  
35 40 45

Leu Tyr Ala Val Arg Ser Glu Arg Lys Leu His Thr Val Gly Asn Leu  
50 55 60

Tyr Ile Val Ser Leu Ser Val Ala Asp Leu Ile Val Gly Ala Val Val  
65 70 75 80

Met Pro Met Asn Ile Leu Tyr Leu Leu Met Ser Lys Trp Ser Leu Gly  
85 90 95

Arg Pro Leu Cys Leu Phe Trp Leu Ser Met Asp Tyr Val Ala Ser Thr  
100 105 110

Ala Ser Ile Phe Ser Val Phe Ile Leu Cys Ile Asp Arg Tyr Arg Ser  
115 120 125

Val Gln Gln Pro Leu Arg Tyr Leu Lys Tyr Arg Thr Lys Thr Arg Ala  
130 135 140

Ser Ala Thr Ile Leu Gly Ala Trp Phe Leu Ser Phe Leu Trp Val Ile  
145 150 155 160

Pro Ile Leu Gly Trp Asn His Phe Met Gln Gln Thr Ser Val Arg Arg  
165 170 175

Glu Asp Lys Cys Glu Thr Asp Phe Tyr Asp Val Thr Trp Phe Lys Val  
180 185 190

Met Thr Ala Ile Ile Asn Phe Tyr Leu Pro Thr Leu Leu Met Leu Trp  
195 200 205

Phe Tyr Ala Lys Ile Tyr Lys Ala Val Arg Gln His Cys Gln His Arg  
210 215 220

Glu Leu Ile Asn Arg Ser Leu Pro Ser Phe Ser Glu Ile Lys Leu Arg

225		230		235		240									
Pro	Glu	Asn	Pro	Lys	Gly	Asp	Ala	Lys	Lys	Pro	Gly	Lys	Glu	Ser	Pro
				245					250					255	
Trp	Glu	Val	Leu	Lys	Arg	Lys	Pro	Lys	Asp	Ala	Gly	Gly	Gly	Ser	Val
			260					265					270		
Leu	Lys	Ser	Pro	Ser	Gln	Thr	Pro	Lys	Glu	Met	Lys	Ser	Pro	Val	Val
		275					280					285			
Phe	Ser	Gln	Glu	Asp	Asp	Arg	Glu	Val	Asp	Lys	Leu	Tyr	Cys	Phe	Pro
	290					295					300				
Leu	Asp	Ile	Val	His	Met	Gln	Ala	Ala	Ala	Glu	Gly	Ser	Ser	Arg	Asp
305					310					315					320
Tyr	Val	Ala	Val	Asn	Arg	Ser	His	Gly	Gln	Leu	Lys	Thr	Asp	Glu	Gln
				325					330					335	
Gly	Leu	Asn	Thr	His	Gly	Ala	Ser	Glu	Ile	Ser	Glu	Asp	Gln	Met	Leu
			340					345					350		
Gly	Asp	Ser	Gln	Ser	Phe	Ser	Arg	Thr	Asp	Ser	Asp	Thr	Thr	Thr	Glu
		355					360					365			
Thr	Ala	Pro	Gly	Lys	Gly	Lys	Leu	Arg	Ser	Gly	Ser	Asn	Thr	Gly	Leu
	370					375					380				
Asp	Tyr	Ile	Lys	Phe	Thr	Trp	Lys	Arg	Leu	Arg	Ser	His	Ser	Arg	Gln
385					390					395					400
Tyr	Val	Ser	Gly	Leu	His	Met	Asn	Arg	Glu	Arg	Lys	Ala	Ala	Lys	Gln
				405					410					415	
Leu	Gly	Phe	Ile	Met	Ala	Ala	Phe	Ile	Leu	Cys	Trp	Ile	Pro	Tyr	Phe
			420					425					430		
Ile	Phe	Phe	Met	Val	Ile	Ala	Phe	Cys	Lys	Asn	Cys	Cys	Asn	Glu	His
		435					440					445			
Leu	His	Met	Phe	Thr	Ile	Trp	Leu	Gly	Tyr	Ile	Asn	Ser	Thr	Leu	Asn
450						455					460				

Pro Leu Ile Tyr Pro Leu Cys Asn Glu Asn Phe Lys Lys Thr Phe Lys  
 465 470 475 480

Arg Ile Leu His Ile Arg Ser  
 485

<210> 5

<211> 3465

<212> DNA

<213> Homo sapiens

<400> 5

agtattggag tgttacaggg agacatacag gatttaagaa gcccatcatg gagaagacct	60
tcaattacag agataaaaag tttttcttgt gaacaagtta cactagatgg aagataacag	120
actgaggagt gagctgcttc tgactcgatt aaaaagggag tgagccataa ctggcggtctg	180
ctcttgccgc aatgagcctc cccaattcct cctgcctctt agaagacaag atgtgtgagg	240
gcaacaagac cactatggcc agccccagc tgatgccctt ggtggtggtc ctgagcacta	300
tctgcttggg cacagtaggg ctcaacctgc tgggtgctgta tgccgtacgg agtgagcgga	360
agctccacac tgtggggaac ctgtacatcg tcagcctctc ggtggcggac ttgatcgtgg	420
gtgccgtcgt catgcctatg aacatcctct acctgctcat gtccaagtgg tcaactgggcc	480
gtcctctctg cctcttttgg ctttccatgg actatgtggc cagcacagcg tccattttca	540
gtgtcttcat cctgtgcatt gatcgctacc gctctgtcca gcagcccctc aggtacctta	600
agtatcgtac caagaccga gcctcggcca ccattctggg ggccctggttt ctctcttttc	660
tgtgggttat tcccattcta ggctggaatc acttcatgca gcagacctcg gtgcgccgag	720
aggacaagtg tgagacagac ttctatgatg tcacctggtt caaggatcatg actgccatca	780
tcaacttcta cctgcccacc ttgctcatgc tctggttcta tgccaagatc tacaaggccg	840
tacgacaaca ctgccagcac cgggagctca tcaataggtc cctcccttcc ttctcagaaa	900
ttaagctgag gccagagaac cccaaggggg atgccaagaa accaggaag gagtctcct	960
gggaggttct gaaaaggaag ccaaaagatg ctggtggtgg atctgtcttg aagtcacat	1020
cccaaaccac caaggagatg aaatccccag ttgtcttcag ccaagaggat gatagagaag	1080
tagacaaact ctactgcttt ccacttgata ttgagcacat gcaggctgcg gcagagggga	1140
gtagcagga ctatgtagcc gtcaaccgga gccatggcca gctcaagaca gatgagcagg	1200
gcctgaacac acatggggcc agcgagatat cagaggatca gatgttaggt gatagccaat	1260

ccttctctcg	aacggactca	gataccacca	cagagacagc	accaggcaaa	ggcaaattga	1320
ggagtgggtc	taacacaggc	ctggattaca	tcaagtttac	ttggaagagg	ctccgctcgc	1380
attcaagaca	gtatgtatct	gggttgacac	tgaaccgcga	aaggaaggcc	gccaaacagt	1440
tgggttttat	catggcagcc	ttcatcctct	gctggatccc	ttatttcac	ttcttcatgg	1500
tcattgcctt	ctgcaagaac	tggtgcaatg	aacatttgca	catgttcacc	atctggctgg	1560
gctacatcaa	ctccacactg	aacccctca	tctacccctt	gtgcaatgag	aacttcaaga	1620
agacattcaa	gagaattctg	catattcgct	cctaaggag	gctctgaggg	gatgcaacaa	1680
aatgatcctt	atgatgtcca	acaaggaaat	agaggacgaa	ggcctgtgtg	ttgccaggca	1740
ggcacctggg	ctttctggaa	tccaaaccac	agtcttaggg	gcttggtagt	ttggaaagtt	1800
cttaggcacc	atagaagaac	agcagatggc	ggtgatcagc	agagagattg	aactttgagg	1860
aggaagcaga	atctttgcaa	gaaagtcaga	cctgtttctt	gtaactgggt	tcaaaaagaa	1920
aaaaataata	aaaataaaag	agagagagaa	tcagacctgg	gtggaactct	cctgctcctc	1980
aggaactatg	ggagcctcag	actcattgta	attcaagctt	tccgagtcaa	gtgattgaca	2040
actgaagaga	cacgtggcta	gggttccact	ggagaattga	aaaggactct	tgagccctcc	2100
tggaatggag	ctgtataact	gtgcagagac	tttatccatg	ccaatagttg	ctgtccccctt	2160
ccaggggtca	ccttgagagg	catgacagct	gttccacagg	ggctatccct	tctcagaaaa	2220
cttctcttct	gagcctcttt	aacagctttc	tccagaacca	gtgtctgaac	caccctggaa	2280
attctgcctt	attatttctt	actcaaacat	gttttagagt	gatagaaaat	tatgcagctt	2340
gcacacccat	cgtctttaac	cccaaatttc	ctttggctat	taaaaaagt	gtggcaaaag	2400
gcacccctca	aagaaagaga	aatgaaatat	ttttgaatgg	ttgcacgtta	aaaattaaaa	2460
gaaggaatgg	gggcagaatg	ccatattttt	gagggtgtga	ctaggtttat	ctcatttaag	2520
ccccacaaca	ccccacagga	gggtaatttt	ctaactctag	tttgcagagg	agcaaattga	2580
ggttcagcaa	ggtgagagag	gtacccaagg	tcacatagct	agttatgtga	gaaagttaga	2640
gtacagatcc	tctgggggtt	tcagcttatt	gtagcatatt	ttctccgaaa	ggcaaaaatg	2700
tgcctttttg	gccgggcatg	gtagctcaag	cctataatcc	cagcatgttg	agaggctgag	2760
gtgggcagat	catttgaggc	caggagtcca	agaccagtct	ggccaatatg	gagaaacctt	2820
gtctctacta	aaaacacaaa	aattatctgg	gcatgggtgg	gcatgcctgt	agtcccactt	2880
acttgggagg	ccgaggcacg	agaatcgctt	gaacccggga	ggtggagggt	gccgtgagcc	2940

aagatcacgc cactgcactc cagcctgggc aacagagcaa gactctgtct caaaaaaaaa	3000
aaatacaata ttttaacaat gtgccctctt aagtgtgcac agatacacat acacggtatt	3060
cccaagagtg gtggcagctc aaaatgatat gtttgagtag acgaacagcc gacatggagt	3120
tcccgtgcac ctacggaagg ggacgctttg aaggaaccaa gtgcattttt atctgtgagt	3180
tctgttgtgt ttgtcaaaaa gtcattgtaa tctttcatag ccatacctgg taagcaaaaa	3240
ctagtaaaga cataggaaca tgcagtttta cttggtgttt atgttgcaat ctggttgtga	3300
tttatatttt aaagcttggt gctaaaccac aatatgtata gcacatggag tgccctgtaca	3360
agctgatgtt ttgtattttg tgttcctctt tgcattgatct gtcaaagtga gatattttta	3420
cctgcctaaa atatgatgtt taaaagcata aaaaaaaaaa aaaaa	3465

<210> 6  
 <211> 1418  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (110)..(979)

aactgtgcga accagaccgc gcagccttgc tcagttcagc atagcggagc ggatccgac	60
ggatcggagc acaccggagc aggtcatcgc agaaggcgtc tgcgagacc atg gag aac	118
	Met Glu Asn
	1
gga tac acc tat gaa gat tat aag aac act gca gaa tgg ctt ctg tct	166
Gly Tyr Thr Tyr Glu Asp Tyr Lys Asn Thr Ala Glu Trp Leu Leu Ser	
5 10 15	
cat act aag cac cga cct caa gtt gca ata atc tgt ggt tct gga tta	214
His Thr Lys His Arg Pro Gln Val Ala Ile Ile Cys Gly Ser Gly Leu	
20 25 30 35	
gga ggt ctg act gat aaa tta act cag gcc cag atc ttt gac tac agt	262
Gly Gly Leu Thr Asp Lys Leu Thr Gln Ala Gln Ile Phe Asp Tyr Ser	
40 45 50	
gaa atc ccc aac ttt cct cga agt aca gtg cca ggt cat gct ggc cga	310
Glu Ile Pro Asn Phe Pro Arg Ser Thr Val Pro Gly His Ala Gly Arg	
55 60 65	
ctg gtg ttt ggg ttc ctg aat ggc agg gcc tgt gtg atg atg cag ggc	358
Leu Val Phe Gly Phe Leu Asn Gly Arg Ala Cys Val Met Met Gln Gly	
70 75 80	
agg ttc cac atg tat gaa ggg tac cca ctc tgg aag gtg aca ttc cca	406

Arg	Phe	His	Met	Tyr	Glu	Gly	Tyr	Pro	Leu	Trp	Lys	Val	Thr	Phe	Pro	
85						90					95					
gtg	agg	gtt	ttc	cac	ctt	ctg	ggg	gtg	gac	acc	ctg	gta	gtc	acc	aat	454
Val	Arg	Val	Phe	His	Leu	Leu	Gly	Val	Asp	Thr	Leu	Val	Val	Thr	Asn	
100					105					110					115	
gca	gca	gga	ggg	ctg	aac	ccc	aag	ttt	gag	gtt	gga	gat	atc	atg	ctg	502
Ala	Ala	Gly	Gly	Leu	Asn	Pro	Lys	Phe	Glu	Val	Gly	Asp	Ile	Met	Leu	
				120					125					130		
atc	cgt	gac	cat	atc	aac	cta	cct	ggg	ttc	agt	ggg	cag	aac	cct	ctc	550
Ile	Arg	Asp	His	Ile	Asn	Leu	Pro	Gly	Phe	Ser	Gly	Gln	Asn	Pro	Leu	
			135					140					145			
aga	ggg	ccc	aat	gat	gaa	agg	ttt	gga	gat	cgt	ttc	cct	gcc	atg	tct	598
Arg	Gly	Pro	Asn	Asp	Glu	Arg	Phe	Gly	Asp	Arg	Phe	Pro	Ala	Met	Ser	
		150					155					160				
gat	gcc	tac	gac	cgg	act	atg	agg	cag	agg	gct	ctc	agt	acc	tgg	aaa	646
Asp	Ala	Tyr	Asp	Arg	Thr	Met	Arg	Gln	Arg	Ala	Leu	Ser	Thr	Trp	Lys	
	165					170					175					
caa	atg	ggg	gag	caa	cgt	gag	cta	cag	gaa	ggc	acc	tat	gtg	atg	gtg	694
Gln	Met	Gly	Glu	Gln	Arg	Glu	Leu	Gln	Glu	Gly	Thr	Tyr	Val	Met	Val	
180					185					190					195	
gca	ggc	ccc	agc	ttt	gag	act	gtg	gca	gaa	tgt	cgt	gtg	ctg	cag	aag	742
Ala	Gly	Pro	Ser	Phe	Glu	Thr	Val	Ala	Glu	Cys	Arg	Val	Leu	Gln	Lys	
				200					205					210		
ctg	gga	gca	gac	gct	gtt	ggc	atg	agt	aca	gta	cca	gaa	gtt	atc	gtt	790
Leu	Gly	Ala	Asp	Ala	Val	Gly	Met	Ser	Thr	Val	Pro	Glu	Val	Ile	Val	
			215					220					225			
gca	cgg	cac	tgt	gga	ctt	cga	gtc	ttt	ggc	ttc	tca	ctc	atc	act	aac	838
Ala	Arg	His	Cys	Gly	Leu	Arg	Val	Phe	Gly	Phe	Ser	Leu	Ile	Thr	Asn	
		230					235					240				
aag	gtc	atc	atg	gat	tat	gaa	agc	ctg	gag	aag	gcc	aac	cat	gaa	gaa	886
Lys	Val	Ile	Met	Asp	Tyr	Glu	Ser	Leu	Glu	Lys	Ala	Asn	His	Glu	Glu	
	245					250					255					
gtc	tta	gca	gct	ggc	aaa	caa	gct	gca	cag	aaa	ttg	gaa	cag	ttt	gtc	934
Val	Leu	Ala	Ala	Gly	Lys	Gln	Ala	Ala	Gln	Lys	Leu	Glu	Gln	Phe	Val	
260				265						270					275	
tcc	att	ctt	atg	gcc	agc	att	cca	ctc	cct	gac	aaa	gcc	agt	tga		979
Ser	Ile	Leu	Met	Ala	Ser	Ile	Pro	Leu	Pro	Asp	Lys	Ala	Ser			
				280					285							
cctgccttg	g	agtcgtctg	g	catctcc	cac	acaagac	cca	agtagctg	ct	accttctttg						1039
gccccttg	ct	ggagtc	atgt	gcctctgt	cc	ttaggttg	tga	gcagaa	agga							

agctgggatt acaggtgtga gcatagtgag accttggcgc tacaaaataa agctgttctc 1219  
attcctgttc tttcttacac aagagctgga gcccgtgccc taccacacat ctgtggagat 1279  
gcccgaggatt tgactcgggc cttagaactt tgcatagcag ctgctactag ctctttgaga 1339  
taatacattc cgaggggctc agttctgcct tatctaaatc accagagacc aaacaaggac 1399  
taatccaata cctcttgga 1418

<210> 7  
<211> 289  
<212> PRT  
<213> Homo sapiens

<400> 7

Met Glu Asn Gly Tyr Thr Tyr Glu Asp Tyr Lys Asn Thr Ala Glu Trp  
1 5 10 15

Leu Leu Ser His Thr Lys His Arg Pro Gln Val Ala Ile Ile Cys Gly  
20 25 30

Ser Gly Leu Gly Gly Leu Thr Asp Lys Leu Thr Gln Ala Gln Ile Phe  
35 40 45

Asp Tyr Ser Glu Ile Pro Asn Phe Pro Arg Ser Thr Val Pro Gly His  
50 55 60

Ala Gly Arg Leu Val Phe Gly Phe Leu Asn Gly Arg Ala Cys Val Met  
65 70 75 80

Met Gln Gly Arg Phe His Met Tyr Glu Gly Tyr Pro Leu Trp Lys Val  
85 90 95

Thr Phe Pro Val Arg Val Phe His Leu Leu Gly Val Asp Thr Leu Val  
100 105 110

Val Thr Asn Ala Ala Gly Gly Leu Asn Pro Lys Phe Glu Val Gly Asp  
115 120 125

Ile Met Leu Ile Arg Asp His Ile Asn Leu Pro Gly Phe Ser Gly Gln  
130 135 140

Asn Pro Leu Arg Gly Pro Asn Asp Glu Arg Phe Gly Asp Arg Phe Pro  
145 150 155 160

Ala Met Ser Asp Ala Tyr Asp Arg Thr Met Arg Gln Arg Ala Leu Ser  
165 170 175

Thr Trp Lys Gln Met Gly Glu Gln Arg Glu Leu Gln Glu Gly Thr Tyr  
180 185 190

Val Met Val Ala Gly Pro Ser Phe Glu Thr Val Ala Glu Cys Arg Val  
195 200 205

Leu Gln Lys Leu Gly Ala Asp Ala Val Gly Met Ser Thr Val Pro Glu  
210 215 220

Val Ile Val Ala Arg His Cys Gly Leu Arg Val Phe Gly Phe Ser Leu  
225 230 235 240

Ile Thr Asn Lys Val Ile Met Asp Tyr Glu Ser Leu Glu Lys Ala Asn  
245 250 255

His Glu Glu Val Leu Ala Ala Gly Lys Gln Ala Ala Gln Lys Leu Glu  
260 265 270

Gln Phe Val Ser Ile Leu Met Ala Ser Ile Pro Leu Pro Asp Lys Ala  
275 280 285

Ser

<210> 8  
<211> 4343  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (11)..(1642)

<400> 8  
agatttgata atg ggc tgc att aaa agt aaa gaa aac aaa agt cca gcc 49  
Met Gly Cys Ile Lys Ser Lys Glu Asn Lys Ser Pro Ala  
1 5 10  
att aaa tac aga cct gaa aat act cca gag cct gtc agt aca agt gtg 97  
Ile Lys Tyr Arg Pro Glu Asn Thr Pro Glu Pro Val Ser Thr Ser Val  
15 20 25  
agc cat tat gga gca gaa ccc act aca gtg tca cca tgt ccg tca tct 145



Ser	His	Tyr	Gly	Ala	Glu	Pro	Thr	Thr	Val	Ser	Pro	Cys	Pro	Ser	Ser		
30					35					40					45		
tca	gca	aag	gga	aca	gca	gtt	aat	ttc	agc	agt	ctt	tcc	atg	aca	cca	193	
Ser	Ala	Lys	Gly	Thr	Ala	Val	Asn	Phe	Ser	Ser	Leu	Ser	Met	Thr	Pro		
				50				55					60				
ttt	gga	gga	tcc	tca	ggg	gta	acg	cct	ttt	gga	ggg	gca	tct	tcc	tca	241	
Phe	Gly	Gly	Ser	Ser	Gly	Val	Thr	Pro	Phe	Gly	Gly	Ala	Ser	Ser	Ser		
			65				70					75					
ttt	tca	gtg	gtg	cca	agt	tca	tat	cct	gct	ggg	tta	aca	ggg	ggg	gtt	289	
Phe	Ser	Val	Val	Pro	Ser	Ser	Tyr	Pro	Ala	Gly	Leu	Thr	Gly	Gly	Val		
		80					85					90					
act	ata	ttt	gtg	gcc	tta	tat	gat	tat	gaa	gct	aga	act	aca	gaa	gac	337	
Thr	Ile	Phe	Val	Ala	Leu	Tyr	Asp	Tyr	Glu	Ala	Arg	Thr	Thr	Glu	Asp		
	95					100					105						
ctt	tca	ttt	aag	aag	ggg	gaa	aga	ttt	caa	ata	att	aac	aat	acg	gaa	385	
Leu	Ser	Phe	Lys	Lys	Gly	Glu	Arg	Phe	Gln	Ile	Ile	Asn	Asn	Thr	Glu		
110					115				120						125		
gga	gat	tgg	tgg	gaa	gca	aga	tca	atc	gct	aca	gga	aag	aat	ggg	tat	433	
Gly	Asp	Trp	Trp	Glu	Ala	Arg	Ser	Ile	Ala	Thr	Gly	Lys	Asn	Gly	Tyr		
				130					135					140			
atc	ccg	agc	aat	tat	gta	gcg	cct	gca	gat	tcc	att	cag	gca	gaa	gaa	481	
Ile	Pro	Ser	Asn	Tyr	Val	Ala	Pro	Ala	Asp	Ser	Ile	Gln	Ala	Glu	Glu		
			145					150					155				
tgg	tat	ttt	ggc	aaa	atg	ggg	aga	aaa	gat	gct	gaa	aga	tta	ctt	ttg	529	
Trp	Tyr	Phe	Gly	Lys	Met	Gly	Arg	Lys	Asp	Ala	Glu	Arg	Leu	Leu	Leu		
		160					165					170					
aat	cct	gga	aat	caa	cga	ggg	att	ttc	tta	gta	aga	gag	agt	gaa	aca	577	
Asn	Pro	Gly	Asn	Gln	Arg	Gly	Ile	Phe	Leu	Val	Arg	Glu	Ser	Glu	Thr		
	175					180					185						
act	aaa	ggg	gct	tat	tcc	ctt	tct	att	cgt	gat	tgg	gat	gag	ata	agg	625	
Thr	Lys	Gly	Ala	Tyr	Ser	Leu	Ser	Ile	Arg	Asp	Trp	Asp	Glu	Ile	Arg		
190					195				200						205		
ggg	gac	aat	gtg	aaa	cac	tac	aaa	att	agg	aaa	ctt	gac	aat	ggg	gga	673	
Gly	Asp	Asn	Val	Lys	His	Tyr	Lys	Ile	Arg	Lys	Leu	Asp	Asn	Gly	Gly		
			210						215					220			
tac	tat	atc	aca	acc	aga	gca	caa	ttt	gat	act	ctg	cag	aaa	ttg	gtg	721	
Tyr	Tyr	Ile	Thr	Thr	Arg	Ala	Gln	Phe	Asp	Thr	Leu	Gln	Lys	Leu	Val		
			225					230					235				
aaa	cac	tac	aca	gaa	cat	gct	gat	ggg	tta	tgc	cac	aag	ttg	aca	act	769	
Lys	His	Tyr	Thr	Glu	His	Ala	Asp	Gly	Leu	Cys	His	Lys	Leu	Thr	Thr		
		240					245					250					
gtg	tgt	cca	act	gtg	aaa	cct	cag	act	caa	ggg	cta	gca	aaa	gat	gct	817	
Val	Cys	Pro	Thr	Val	Lys	Pro	Gln	Thr	Gln	Gly	Leu	Ala	Lys	Asp	Ala		

255	260	265	
tgg gaa atc cct cga gaa tct ttg cga cta gag gtt aaa cta gga caa			865
Trp Glu Ile Pro Arg Glu Ser Leu Arg Leu Glu Val Lys Leu Gly Gln			
270	275	280	285
gga tgt ttc ggc gaa gtg tgg atg gga aca tgg aat gga acc acg aaa			913
Gly Cys Phe Gly Glu Val Trp Met Gly Thr Trp Asn Gly Thr Thr Lys			
	290	295	300
gta gca atc aaa aca cta aaa cca ggt aca atg atg cca gaa gct ttc			961
Val Ala Ile Lys Thr Leu Lys Pro Gly Thr Met Met Pro Glu Ala Phe			
	305	310	315
ctt caa gaa gct cag ata atg aaa aaa tta aga cat gat aaa ctt gtt			1009
Leu Gln Glu Ala Gln Ile Met Lys Lys Leu Arg His Asp Lys Leu Val			
	320	325	330
cca cta tat gct gtt gtt tct gaa gaa cca att tac att gtc act gaa			1057
Pro Leu Tyr Ala Val Val Ser Glu Glu Pro Ile Tyr Ile Val Thr Glu			
	335	340	345
ttt atg tca aaa gga agc tta tta gat ttc ctt aag gaa gga gat gga			1105
Phe Met Ser Lys Gly Ser Leu Leu Asp Phe Leu Lys Glu Gly Asp Gly			
	350	355	360
aag tat ttg aag ctt cca cag ctg gtt gat atg gct gct cag att gct			1153
Lys Tyr Leu Lys Leu Pro Gln Leu Val Asp Met Ala Ala Gln Ile Ala			
	370	375	380
gat ggt atg gca tat att gaa aga atg aac tat att cac cga gat ctt			1201
Asp Gly Met Ala Tyr Ile Glu Arg Met Asn Tyr Ile His Arg Asp Leu			
	385	390	395
cgg gct gct aat att ctt gta gga gaa aat ctt gtg tgc aaa ata gca			1249
Arg Ala Ala Asn Ile Leu Val Gly Glu Asn Leu Val Cys Lys Ile Ala			
	400	405	410
gac ttt ggt tta gca agg tta att gaa gac aat gaa tac aca gca aga			1297
Asp Phe Gly Leu Ala Arg Leu Ile Glu Asp Asn Glu Tyr Thr Ala Arg			
	415	420	425
caa ggt gca aaa ttt cca atc aaa tgg aca gct cct gaa gct gca ctg			1345
Gln Gly Ala Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ala Leu			
	430	435	440
tat ggt cgg ttt aca ata aag tct gat gtc tgg tca ttt gga att ctg			1393
Tyr Gly Arg Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu			
	450	455	460
caa aca gaa cta gta aca aag ggc cga gtg cca tat cca ggt atg gtg			1441
Gln Thr Glu Leu Val Thr Lys Gly Arg Val Pro Tyr Pro Gly Met Val			
	465	470	475
aac cgt gaa gta cta gaa caa gtg gag cga gga tac agg atg ccg tgc			1489
Asn Arg Glu Val Leu Glu Gln Val Glu Arg Gly Tyr Arg Met Pro Cys			
	480	485	490

cct cag ggc tgt cca gaa tcc ctc cat gaa ttg atg aat ctg tgt tgg	1537
Pro Gln Gly Cys Pro Glu Ser Leu His Glu Leu Met Asn Leu Cys Trp	
495 500 505	
aag aag gac cct gat gaa aga cca aca ttt gaa tat att cag tcc ttc	1585
Lys Lys Asp Pro Asp Glu Arg Pro Thr Phe Glu Tyr Ile Gln Ser Phe	
510 515 520 525	
ttg gaa gac tac ttc act gct aca gag cca cag tac cag cca gga gaa	1633
Leu Glu Asp Tyr Phe Thr Ala Thr Glu Pro Gln Tyr Gln Pro Gly Glu	
530 535 540	
aat tta taa ttcaagtagc ctattttata tgcacaaatc tgccaaaata	1682
Asn Leu	
taaagaactt gtgtagattt tctacaggaa tcaaaagaag aaaatcttct ttactctgca	1742
tgtttttaaat ggtaaactgg aatcccagat atgggtgcac aaaaccactt ttttttcccc	1802
aagtattaaa ctctaata gta ccaatgatga atttatcagc gtatttcagg gtccaaacaa	1862
aatagagcta agatactgat gacagtgtgg gtgacagcat ggtaatgaag gacagtgagg	1922
ctcctgctta ttataaaatc atttcctttc tttttttccc caaagtcaga attgctcaaa	1982
gaaaattatt tattgttaca gataaaactt gagagataaa aagctatacc ataataaaat	2042
ctaaaattaa ggaatatcat gggaccaa atattccattc cagtttttta aagtttcttg	2102
catttattat tctcaaaagt tttttctaag ttaaacagtc agtatgcaat cttaatatat	2162
gctttctttt gcatggacat gggccagggt tttcaaaagg aatataaaca ggatctcaaa	2222
cttgattaaa tgtagacca cagaagtggg atttgaaagt ataatgcagt acattaatat	2282
tcatgttcat ggaactgaaa gaataagaac tttttcactt cagtcctttt ctgaagagtt	2342
tgacttagaa taatgaagg aactagaaag tgagttaatc ttgtatgagg ttgcattgat	2402
tttttaaggc aatatataat tgaaactact gtccaatcaa aggggaaatg ttttgatctt	2462
tagatagcat gcaaagtaag acccagcatt ttaaaagccc tttttaaaaa ctagacttcg	2522
tactgtgagt attgcttata tgtccttatg gggatgggtg ccacaaatag aaaatatgac	2582
cagatcaggg acttgaatgc acttttgctc atgggtgaata tagatgaaca gagaggaaaa	2642
tgtattttaa agaaatacga gaaaagaaaa tgtgaaagtt ttacaagtta gagggatgga	2702
aggtaatgtt taatgttgat gtcatggagt gacagaatgg ctttgctggc actcagagct	2762
cctcacttag ctatattctg agactttgaa gagttataaa gtataactat aaaactaatt	2822
tttcttacac actaaatggg tatttgttca aaataatgaa gttatggctt cacattcatt	2882

gcagtgggat atgggttttta tgtaaaacat ttttagaact ccagttttca aatcatgttt	2942
gaatctacat tcactttttt ttgttttctt ttttgagacg gagtctcgct ctgccgcca	3002
ggctggagtg cagtggcgcg atctcggtc actgcaagct ctgcctccca ggttcacacc	3062
attctcctgc ctcagcctcc cgagtagctg ggactacagg tgcccaccac cacgcctggc	3122
tagttttttg tatttttagt agagacgcag tttcacctg ttagccagga tggctctgat	3182
ctcctgacct tgtgatctgc ccgcctcggc ctcccaaagt gctgggatta caggcgtgag	3242
ccaccgcgcc cagcctacat tcacttctaa agtctatgta atgggtggta ttttttcct	3302
tttagaatac attaaatggg tgatttgggg aggaaaactt attctgaata ttaacgggtg	3362
tgaaaagggg acagttttta ccctaaagtg caaaagtga acatacaaaa taagactaat	3422
ttttaagagt aactcagtaa tttcaaaata cagatttgaa tagcagcatt agtggtttga	3482
gtgtctagca aaggaaaaat tgatgaataa aatgaaggtc tgggtgtatat gttttaaaat	3542
actctcatat agtcacactt taaattaagc cttatattag gcccctctat tttcaggata	3602
taattcttaa ctatcattat ttacctgatt ttaatcatca gattcgaaat tctgtgcat	3662
ggcgtatatg ttcaaattca aaccattttt aaaatgtgaa gatggacttc atgcaagttg	3722
gcagtgggtc tgggtactaaa aattgtgggt gttttttctg tttacgtaac ctgcttagta	3782
ttgacactct ctaccaagag ggtcttccta agaagagtgc tgtcattatt tcctcttacc	3842
aacaacttgt gacatgagat tttttaaggg ctttatgtga actatgatat tgtaattttt	3902
ctaagcatat tcaaaagggt gacaaaatta cgtttatgta ctaaactctaa tcaggaaagt	3962
aaggcaggaa aagttgatgg tattcattag gttttaactg aatggagcag ttccttatat	4022
aataacaatt gtatagtagg gataaaacac taacttaatg tgtattcatt ttaaattggt	4082
ctgtattttt aaattgccaa gaaaaacaac tttgtaaatt tggagatatt ttccaacagc	4142
ttttcgtctt cagtgtctta atgtggaagt taacccttac caaaaaagga agttggcaaa	4202
aacagccttc tagcacactt ttttaaatga ataatggtag cctaaactta atatttttat	4262
aaagtattgt aatattgttt tgtggataat tgaaataaaa agttctcatt gaatgcacct	4322
attaaaaaaaa aaaaaaaaaa a	4343

<210> 9  
 <211> 543  
 <212> PRT  
 <213> Homo sapiens  
 <400> 9

Met Gly Cys Ile Lys Ser Lys Glu Asn Lys Ser Pro Ala Ile Lys Tyr  
1 5 10 15

Arg Pro Glu Asn Thr Pro Glu Pro Val Ser Thr Ser Val Ser His Tyr  
20 25 30

Gly Ala Glu Pro Thr Thr Val Ser Pro Cys Pro Ser Ser Ser Ala Lys  
35 40 45

Gly Thr Ala Val Asn Phe Ser Ser Leu Ser Met Thr Pro Phe Gly Gly  
50 55 60

Ser Ser Gly Val Thr Pro Phe Gly Gly Ala Ser Ser Ser Phe Ser Val  
65 70 75 80

Val Pro Ser Ser Tyr Pro Ala Gly Leu Thr Gly Gly Val Thr Ile Phe  
85 90 95

Val Ala Leu Tyr Asp Tyr Glu Ala Arg Thr Thr Glu Asp Leu Ser Phe  
100 105 110

Lys Lys Gly Glu Arg Phe Gln Ile Ile Asn Asn Thr Glu Gly Asp Trp  
115 120 125

Trp Glu Ala Arg Ser Ile Ala Thr Gly Lys Asn Gly Tyr Ile Pro Ser  
130 135 140

Asn Tyr Val Ala Pro Ala Asp Ser Ile Gln Ala Glu Glu Trp Tyr Phe  
145 150 155 160

Gly Lys Met Gly Arg Lys Asp Ala Glu Arg Leu Leu Leu Asn Pro Gly  
165 170 175

Asn Gln Arg Gly Ile Phe Leu Val Arg Glu Ser Glu Thr Thr Lys Gly  
180 185 190

Ala Tyr Ser Leu Ser Ile Arg Asp Trp Asp Glu Ile Arg Gly Asp Asn  
195 200 205

Val Lys His Tyr Lys Ile Arg Lys Leu Asp Asn Gly Gly Tyr Tyr Ile  
210 215 220

Thr Thr Arg Ala Gln Phe Asp Thr Leu Gln Lys Leu Val Lys His Tyr  
225 230 235 240

Thr Glu His Ala Asp Gly Leu Cys His Lys Leu Thr Thr Val Cys Pro  
245 250 255

Thr Val Lys Pro Gln Thr Gln Gly Leu Ala Lys Asp Ala Trp Glu Ile  
260 265 270

Pro Arg Glu Ser Leu Arg Leu Glu Val Lys Leu Gly Gln Gly Cys Phe  
275 280 285

Gly Glu Val Trp Met Gly Thr Trp Asn Gly Thr Thr Lys Val Ala Ile  
290 295 300

Lys Thr Leu Lys Pro Gly Thr Met Met Pro Glu Ala Phe Leu Gln Glu  
305 310 315 320

Ala Gln Ile Met Lys Lys Leu Arg His Asp Lys Leu Val Pro Leu Tyr  
325 330 335

Ala Val Val Ser Glu Glu Pro Ile Tyr Ile Val Thr Glu Phe Met Ser  
340 345 350

Lys Gly Ser Leu Leu Asp Phe Leu Lys Glu Gly Asp Gly Lys Tyr Leu  
355 360 365

Lys Leu Pro Gln Leu Val Asp Met Ala Ala Gln Ile Ala Asp Gly Met  
370 375 380

Ala Tyr Ile Glu Arg Met Asn Tyr Ile His Arg Asp Leu Arg Ala Ala  
385 390 395 400

Asn Ile Leu Val Gly Glu Asn Leu Val Cys Lys Ile Ala Asp Phe Gly  
405 410 415

Leu Ala Arg Leu Ile Glu Asp Asn Glu Tyr Thr Ala Arg Gln Gly Ala  
420 425 430

Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ala Leu Tyr Gly Arg  
435 440 445

Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Gln Thr Glu

450

455

460

Leu Val Thr Lys Gly Arg Val Pro Tyr Pro Gly Met Val Asn Arg Glu  
 465 470 475 480

Val Leu Glu Gln Val Glu Arg Gly Tyr Arg Met Pro Cys Pro Gln Gly  
 485 490 495

Cys Pro Glu Ser Leu His Glu Leu Met Asn Leu Cys Trp Lys Lys Asp  
 500 505 510

Pro Asp Glu Arg Pro Thr Phe Glu Tyr Ile Gln Ser Phe Leu Glu Asp  
 515 520 525

Tyr Phe Thr Ala Thr Glu Pro Gln Tyr Gln Pro Gly Glu Asn Leu  
 530 535 540

&lt;210&gt; 10

&lt;211&gt; 25

&lt;212&gt; DNA

&lt;213&gt; artificial sequence

&lt;220&gt;

&lt;223&gt; HMG20B PMO antisense oligomer

&lt;400&gt; 10

cgcccagcat cttggtgatc tcggg

25

&lt;210&gt; 11

&lt;211&gt; 25

&lt;212&gt; DNA

&lt;213&gt; artificial sequence

&lt;220&gt;

&lt;223&gt; HRH1-specific PMO antisense oligo

&lt;400&gt; 11

gcgaaagagc agccgccagt tatgg

25

&lt;210&gt; 12

&lt;211&gt; 25

&lt;212&gt; DNA

&lt;213&gt; artificial sequence

&lt;220&gt;

&lt;223&gt; NP-specific PMO antisense oligo

&lt;400&gt; 12

cttcataggt gtatccgttc tccat

25

<210> 13  
 <211> 25  
 <212> DNA  
 <213> artificial sequence  
  
 <220>  
 <223> YES-specific PMO antisense oligo  
  
 <400> 13  
 tttctttact tttaatgcag cccat 25

<210> 14  
 <211> 25  
 <212> DNA  
 <213> artificial sequence  
  
 <220>  
 <223> ARF1-specific PMO antisense oligo  
  
 <400> 14  
 atgcttgtgg acaggtggaa ggaca 25

<210> 15  
 <211> 21  
 <212> RNA  
 <213> Homo sapiens  
  
 <400> 15  
 aacgccuuuu ggaggugcau c 21

<210> 16  
 <211> 21  
 <212> RNA  
 <213> Homo sapiens  
  
 <400> 16  
 aacgccuuuu ggaggugcau c 21

<210> 17  
 <211> 4343  
 <212> RNA  
 <213> Homo sapiens  
  
 <220>  
 <221> misc\_feature  
 <222> (214)..(234)  
 <223> region corresponding to siRNA-214  
  
 <220>  
 <221> misc\_feature



<222> (318)..(338)

<223> region corresponding to siRNA-318

<400> 17

agauuugaua	augggcugca	uuaaaaguaa	agaaaacaaa	aguccagcca	uuaaauacag	60
accugaaaau	acuccagagc	cugucaguac	aagugugagc	cauuauaggag	cagaacccac	120
uacaguguca	ccauguccgu	caucuucagc	aaagggaaaca	gcaguuaauu	ucagcagucu	180
uuccaugaca	ccauuuggag	gauccucagg	gguaacgccu	uuuggaggug	caucuuccuc	240
auuuucagug	gugccaaguu	cauauccugc	ugguuuuaca	ggugguguuu	cuauauuugu	300
ggccuuauau	gauuaugaag	cuagaacuac	agaagaccuu	ucauuuaaga	agggugaaag	360
auuucaaaau	auuaacaaua	cggaggaga	uuggugggaa	gcaagaucaa	ucgcuacagg	420
aaagaauugu	uauaucccga	gcauuuauu	agcgccugca	gauuccauuc	aggcagaaga	480
augguauuuu	ggcaaaaugg	ggagaaaaga	ugcugaaaga	uuacuuuuga	auccuggaaa	540
ucaacgaggu	auuuucuuag	uaagagagag	ugaaacaacu	aaaggugcuu	auucccuuuc	600
uauucgugau	ugggauagaga	uaagggguga	caaugugaaa	cacuacaaaa	uuaggaaacu	660
ugacaauugu	ggauacuaua	ucacaaccag	agcacaauuu	gauacucugc	agaaauuggu	720
gaaacacuac	acagaacaug	cugaugguuu	augccacaag	uugacaacug	uguguccaac	780
ugugaaaccu	cagacucaag	gucuagcaaa	agaugcuugg	gaaaucccuc	gagaauuuu	840
gcgacuagag	guuaaacuag	gacaaggau	uuucggcgaa	guguggaugg	gaacauggaa	900
uggaaccacg	aaaguagcaa	ucaaaacacu	aaaaccaggu	acaauaugc	cagaagcuuu	960
ccuuaagaa	gcucagauaa	ugaaaaaaau	aagacaugau	aaacuuguuc	cacuauaugc	1020
uguuguuucu	gaagaaccaa	uuuacauugu	cacugaauuu	auguacaaaag	gaagcuuauu	1080
agauuuccuu	aaggaaggag	auggaaagua	uuugaagcuu	ccacagcugg	uugauauggc	1140
ugcucagauu	gcugauggua	uggcauauau	ugaaagaau	aacuauauuc	accgagaucu	1200
ucgggcugcu	aaauuucuug	uaggagaaaa	ucuugugugc	aaaauagcag	acuuugguuu	1260
agcaaggguu	auugaagaca	augaauacac	agcaagacaa	ggugcaaaaau	uuccaaucua	1320
auggacagcu	ccugaagcug	cacuguaugg	ucgguuuaca	auaaagucug	augucugguc	1380
auuuggaauu	cugcaaacag	aacuaguaac	aaagggccga	gugccauauc	cagguauggu	1440
gaaccgugaa	guacuagaac	aaguggagcg	aggauacagg	augccgugcc	cucagggcug	1500
uccagaaucc	cuccaugaau	ugaugaauuc	guguuggaag	aaggaccucg	augaaagacc	1560
aacauugaa	uauauucagu	ccuucuugga	agacuacuuc	acugcuacag	agccacagua	1620

ccagccagga	gaaaauuuau	aaaucaagua	gccuauuuua	uaugcacaaa	ucugccaaaa	1680
uauaaagaac	uuguguagau	uuucuaacagg	aaucaaaaga	agaaaaucuu	cuuuacucug	1740
cauguuuuuu	augguaaacu	ggaaucccag	auaugguugc	acaaaaccac	uuuuuuuucc	1800
ccaaguauua	aacucuaaug	uaccaaugau	gaauuuauca	gcguauuuca	ggguccaaac	1860
aaaauagagc	uaagauacug	augacagugu	gggugacagc	augguaauga	aggacaguga	1920
ggcuccugcu	uauuuauaaa	ucauuuccuu	ucuuuuuuuc	cccaaaguca	gaauugcuca	1980
aagaaaauuu	uuuauuguua	cagauaaaac	uugagagaua	aaaagcuaua	ccauaauaaa	2040
aucuaaaauu	aaggaauauc	augggacca	auaaauccau	uccaguuuuu	uaaaguuuu	2100
ugcauuuauu	auucucaaaa	guuuuuucua	aguuaaacag	ucaguaugca	aucuuauau	2160
augcuuucuu	uugcauggac	augggccagg	uuuuucaaaa	ggaauauaaa	caggauucu	2220
aacuugauua	aauguuagac	cacagaagug	gaauuugaaa	guauaaugca	guacauuaa	2280
auucauguuc	auggaacuga	aagaauaaga	acuuuuucac	uucaguccuu	uucugaagag	2340
uuugacuuag	aaauaagaag	guaacuagaa	agugaguuaa	ucuuguauga	ggugcauug	2400
auuuuuuaag	gcaauauaua	auugaaacua	cuguccaauc	aaaggggaaa	uguuuugauc	2460
uuuagauagc	augcaaagua	agaccagca	uuuuaaaagc	ccuuuuuuaa	aacuagacuu	2520
cguacuguga	guauugcuua	uauugccuua	uggggauggg	ugccacaaau	agaaaauaug	2580
accagaucag	ggacuugaau	gcacuuuugc	ucauggugaa	uauagaugaa	cagagaggaa	2640
aauguauuuu	aaagaaauac	gagaaaagaa	aaugugaaag	uuuuacaagu	uagagggaug	2700
gaagguaaug	uuuaauguug	augucaugga	gugacagaau	ggcuuugcug	gcacucagag	2760
cuccucacuu	agcuauauuc	ugagacuug	aagaguuaa	aaguauaacu	auaaaacuaa	2820
uuuuucuuac	acacuaaaug	gguaauuguu	caaaauaaug	aaguuauggc	uucacauuca	2880
uugcaguggg	auaugguuuu	uauguaaaac	auuuuuagaa	cuccaguuuu	caaaucaugu	2940
uugaaucuac	auucacuuuu	uuuuguuuuc	uuuuuugaga	cggagucucg	cucugccgcc	3000
caggcuggag	ugcaguggcg	cgaucucggc	ucacugcaag	cucugccucc	cagguucaca	3060
ccaauucuccu	gccucagccu	cccagaguagc	ugggacuaca	ggugcccacc	accacgccug	3120
gcuaguuuuu	uguauuuuuu	guagagacgc	aguuuaccgc	uguuagccag	gauggucucg	3180
aucuccugac	cuugugaucu	gcccgcucgc	gccucccaaa	gugcugggau	uacagggcug	3240
agccaccgcg	cccagccuac	auucacuucu	aaagucuaug	uauggguggu	cauuuuuucc	3300

cuuuuagaau	acauuaaaug	guugauuugg	ggaggaaaac	uuauucugaa	uauuaacggu	3360
ggugaaaagg	ggacaguuuu	uacccuaaag	ugcaaaagug	aaacauacaa	aaauagacua	3420
auuuuuuaga	guaacucagu	aauuucaaaa	uacagauuug	aaauagcagca	uuagugguuu	3480
gagugucuag	caaaggaaaa	auugaugaau	aaaaugaagg	ucugguguaa	auguuuuaaa	3540
auacucucau	auagucacac	uuuaaaauaa	gccuuauuu	aggccccucu	auuuucagga	3600
uauaaauucu	aacuaucuu	auuuaccuga	uuuaaucau	cagauucgaa	auucugugcc	3660
auggcguaua	uguucaaau	caaaccuuu	uuaaaugug	aagauggacu	ucaugcaagu	3720
uggcaguggu	ucugguacua	aaaauugugg	uuguuuuuuc	uguuuacgua	accugcuuag	3780
uauugacacu	cucuaccaag	aggguuuucc	uaagaagagu	gcugucauua	uuuccucuua	3840
ucaacaacuu	gugacaugag	auuuuuuaag	ggcuuuuangu	gaacuaugau	auuguaauuu	3900
uucuaagcau	auucaaaagg	gugacaaaau	uacguuuuug	uacuaaaucu	aaucaggaaa	3960
guaaggcagg	aaaaguugau	gguaaucauu	agguuuuaac	ugaauaggagc	aguuccuuau	4020
auaauaacia	uuguauagua	gggauaaaaac	acuaacuuaa	uguguauuca	uuuuaaaauug	4080
uucuguauuu	uuaaaauugcc	aagaaaaaca	acuuuguuaa	uuuggagaua	uuuuccaaca	4140
gcuuuucguc	uucagugucu	uaauguggaa	guuaaccuuu	accaaaaaag	gaaguuggca	4200
aaaacagccu	ucuagcacac	uuuuuuuuuu	gaauaauggu	agccuaaacu	uaauuuuuuu	4260
auaaaguauu	guaauauugu	uuuguggaua	auugaaauaa	aaaguucuca	uugaaugcac	4320
cuauuaaaaa	aaaaaaaaaa	aaa				4343